

**PALM INTRANET**Day : Tuesday
Date: 10/17/2006

Time: 10:11:47

10/17/2006

Inventor Name Search

Enter the **first few letters** of the Inventor's Last Name.

Additionally, enter the **first few letters** of the Inventor's First name.

Last Name**First Name**

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PALM INTRANETDay : Tuesday
Date: 10/17/2006

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10/17/96

Inventor Name SearchEnter the **first few letters** of the Inventor's Last Name.Additionally, enter the **first few letters** of the Inventor's First name.**Last Name****First Name**

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SCORE Search Results Details for Application 10717296 and Search Result us-10-717-296- 307.rag.

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OM protein - protein search, using sw model

Run on: October 14, 2006, 10:08:40 ; Search time 198 Seconds
(without alignments)
1166.133 Million cell updates/sec

Title: US-10-717-296-307
Perfect score: 2690
Sequence: 1 MEPSWLQELMAHPFLLL.....VRQVVLKSKNGIHVFAKKVC 505

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	2690	100.0	505	5	AAE14447	Aae14447 Human dru
3	2690	100.0	505	5	ADU01526	Adu01526 Breast ca
4	2690	100.0	505	5	ADZ41790	Adz41790 Human bre
5	2685	99.8	505	5	AAU83606	Aau83606 Human PRO
6	2685	99.8	505	5	ADY31770	Ady31770 Novel hum
7	2685	99.8	505	6	ABU10221	Abu10221 Human cyt
8	2685	99.8	505	6	ABU80753	Abu80753 Human PRO
9	2685	99.8	505	6	ABO33719	Abo33719 Novel hum
10	2685	99.8	505	6	ABU82062	Abu82062 Novel hum
11	2685	99.8	505	6	ABJ72242	Abj72242 Human PRO
12	2685	99.8	505	6	ABJ72370	Abj72370 Human PRO
13	2685	99.8	505	6	ABO34265	Abo34265 Human sec
14	2685	99.8	505	7	ABJ72072	Abj72072 Human mem
15	2685	99.8	505	7	ADB83520	Adb83520 Novel hum
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17	2685	99.8	505	7	ADB73167	Adb73167 Novel hum
18	2685	99.8	505	7	ADB78249	Adb78249 Novel hum
19	2685	99.8	505	7	ADB84897	Adb84897 Human PRO
20	2685	99.8	505	7	ADB78003	Adb78003 Novel hum
21	2685	99.8	505	7	ADB87069	Adb87069 Human PRO
22	2685	99.8	505	7	ADB84651	Adb84651 Human PRO
23	2685	99.8	505	7	ADB83766	Adb83766 Novel hum
24	2685	99.8	505	7	ADB72921	Adb72921 Novel hum
25	2685	99.8	505	7	ADC36759	Adc36759 Human PRO
26	2685	99.8	505	7	ADC21749	Adc21749 Human PRO
27	2685	99.8	505	7	AAE39879	Aae39879 Human cyt
28	2685	99.8	505	7	ADC49780	Adc49780 Novel hum
29	2685	99.8	505	7	ADC48979	Adc48979 Novel hum
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32	2685	99.8	505	7	ADC47102	Adc47102 Novel hum
33	2685	99.8	505	7	ADC77977	Adc77977 Novel hum
34	2685	99.8	505	7	ADD06212	Add06212 Novel hum
35	2685	99.8	505	7	ADC77731	Adc77731 Novel hum
36	2685	99.8	505	7	ADD50694	Add50694 Novel hum
37	2685	99.8	505	7	ADD50940	Add50940 Novel hum
38	2685	99.8	505	7	ADD50421	Add50421 Human PRO
39	2685	99.8	505	7	ADD50175	Add50175 Human PRO
40	2685	99.8	505	7	ADD51186	Add51186 Novel hum
41	2685	99.8	505	8	ADC48733	Adc48733 Novel hum
42	2685	99.8	505	8	ADE20904	Ade20904 Novel hum
43	2685	99.8	505	8	ADE05748	Ade05748 Human PRO
44	2685	99.8	505	8	ADD74977	Add74977 Human PRO
45	2685	99.8	505	8	ADD75723	Add75723 Novel hum

ALIGNMENTS

RESULT 1
 ABJ05536
 ID ABJ05536 standard; protein; 505 AA.
 XX
 AC ABJ05536;
 XX
 DT 14-NOV-2002 (first entry)

SCORE Search Results Details for Application 10717296 and Search Result us-10-717-296- 307.rai.

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OM protein - protein search, using sw model

Run on: October 14, 2006, 10:18:25 ; Search time 52 Seconds
(without alignments)
850.057 Million cell updates/sec

Title: US-10-717-296-307

Perfect score: 2690

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Scoring table: BLOSUM62

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Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summarie

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1465.5	54.5	510	2	US-09-852-067-2	Sequence 2, Appli
2	1465.5	54.5	510	2	US-10-338-691-2	Sequence 2, Appli
3	1391	51.7	489	2	US-09-852-067-4	Sequence 4, Appli
4	1391	51.7	489	2	US-10-338-691-4	Sequence 4, Appli
5	1310	48.7	444	2	US-10-104-047-2690	Sequence 2690, Ap
6	1017	37.8	520	3	US-10-114-270-60	Sequence 60, Appl
7	1005	37.4	524	2	US-09-976-594-533	Sequence 533, App
8	994	37.0	524	2	US-09-991-181-264	Sequence 264, App
9	994	37.0	524	2	US-09-990-444-264	Sequence 264, App
10	994	37.0	524	2	US-09-997-333-264	Sequence 264, App
11	994	37.0	524	2	US-09-992-598-264	Sequence 264, App
12	994	37.0	524	2	US-09-989-735-264	Sequence 264, App
13	994	37.0	524	3	US-09-989-726-264	Sequence 264, App
14	994	37.0	524	3	US-09-997-514-264	Sequence 264, App
15	994	37.0	524	3	US-09-989-728-264	Sequence 264, App
16	994	37.0	524	3	US-09-997-349-264	Sequence 264, App
17	994	37.0	524	3	US-09-997-653-264	Sequence 264, App
18	994	37.0	524	3	US-09-989-293A-264	Sequence 264, App
19	974.5	36.2	527	2	US-09-949-016-10078	Sequence 10078, A
20	966	35.9	520	2	US-09-949-016-6003	Sequence 6003, Ap
21	651.5	24.2	314	2	US-10-104-047-2794	Sequence 2794, Ap
22	543.5	20.2	520	2	US-09-527-073-2	Sequence 2, Appli
23	543.5	20.2	520	3	US-09-992-901-2	Sequence 2, Appli
24	487.5	18.1	503	2	US-09-583-447A-2	Sequence 2, Appli
25	478.5	17.8	508	2	US-09-949-016-8561	Sequence 8561, Ap
26	478	17.8	504	2	US-09-583-447A-4	Sequence 4, Appli
27	469.5	17.5	508	2	US-09-949-016-7092	Sequence 7092, Ap
28	469.5	17.5	508	2	US-09-949-016-8562	Sequence 8562, Ap
29	464	17.2	504	2	US-09-502-426B-24	Sequence 24, Appl
30	463.5	17.2	503	2	US-09-144-367-2	Sequence 2, Appli
31	437	16.2	502	2	US-09-949-016-5992	Sequence 5992, Ap
32	437	16.2	507	2	US-09-949-016-7091	Sequence 7091, Ap
33	430	16.0	576	2	US-08-948-564-16	Sequence 16, Appl
34	416.5	15.5	504	1	US-08-457-274A-25	Sequence 25, Appl
35	416.5	15.5	504	5	PCT-US95-05758-25	Sequence 25, Appl
36	413	15.4	510	3	US-10-021-425-36	Sequence 36, Appl
37	389	14.5	526	1	US-08-298-426-4	Sequence 4, Appli
38	385.5	14.3	498	1	US-08-457-274A-24	Sequence 24, Appl
39	385.5	14.3	498	5	PCT-US95-05758-24	Sequence 24, Appl
40	378	14.1	512	2	US-09-270-767-45399	Sequence 45399, A
41	370	13.8	507	1	US-08-457-274A-23	Sequence 23, Appl
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44	360	13.4	1049	2	US-10-018-730A-4	Sequence 4, Appli
45	359.5	13.4	420	2	US-09-583-447A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-852-067-2

; Sequence 2, Application US/09852067
; Patent No. 6531297
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF

SCORE Search Results Details for Application 10717296 and Search Result us-10-717-296- 307.rapbm.

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OM protein - protein search, using sw model

Run on: October 14, 2006, 10:19:10 ; Search time 188 Seconds
(without alignments)
1244.274 Million cell updates/sec

Title: US-10-717-296-307

Perfect score: 2690

Sequence: 1 MEPSWLQELMAHPFLLLILL.....VRQVVLKSKNGIHVFAKKVC 505

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Query Score	Match Length	DB ID	Description
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3	2690	100.0	505	4	US-10-058-270A-2	Sequence 2, Appl
4	2690	100.0	505	4	US-10-296-606-10	Sequence 10, Appl
5	2690	100.0	505	4	US-10-717-296-307	Sequence 307, App
6	2685	99.8	505	4	US-10-067-668-2	Sequence 2, Appl
7	2685	99.8	505	4	US-10-227-884-30	Sequence 30, Appl
8	2685	99.8	505	4	US-10-230-163-30	Sequence 30, Appl
9	2685	99.8	505	4	US-10-230-338-30	Sequence 30, Appl
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15	2685	99.8	505	4	US-10-227-873-30	Sequence 30, Appl
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28	2685	99.8	505	4	US-10-175-696-2	Sequence 2, Appl
29	2685	99.8	505	4	US-10-216-165-30	Sequence 30, Appl
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33	2685	99.8	505	4	US-10-219-536-30	Sequence 30, Appl
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ALIGNMENTS

RESULT 1

US-09-910-689-307

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; Sequence 307, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
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SCORE Search Results Details for Application 10717296 and Search Result us-10-717-296- 307.rapbn.

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OM protein - protein search, using sw model

Run on: October 14, 2006, 10:20:10 ; Search time 39 Seconds
(without alignments)
1028.197 Million cell updates/sec

Title: US-10-717-296-307

Perfect score: 2690

Sequence: 1 MEPSWLQELMAHPFLLLILL VRQVVLKSKNIGHVFAKKVC 505

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 295242 seqs, 79405279 residues

Total number of hits satisfying chosen parameters: 295242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match Length	DB	ID	Description
1	2685	99.8	505	6 US-10-540-310-4	Sequence 4, Appli
2	1727	64.2	340	7 US-11-293-697-4300	Sequence 4300, Ap
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4	1349	50.1	508	7 US-11-293-697-4775	Sequence 4775, Ap
5	1236.5	46.0	511	7 US-11-090-997-136	Sequence 136, App
6	1180.5	43.9	511	7 US-11-090-997-1026	Sequence 1026, Ap
7	994	37.0	524	6 US-10-196-749-204	Sequence 204, App
8	994	37.0	524	7 US-11-101-316-54	Sequence 54, Appl
9	994	37.0	524	7 US-11-376-673-54	Sequence 54, Appl
10	973	36.2	531	7 US-11-293-697-3957	Sequence 3957, Ap
11	543.5	20.2	520	7 US-11-056-355B-49170	Sequence 49170, A
12	538	20.0	493	7 US-11-056-355B-49171	Sequence 49171, A
13	525.5	19.5	456	7 US-11-056-355B-49172	Sequence 49172, A
14	487.5	18.1	503	6 US-10-532-868-13	Sequence 13, Appl
15	478.5	17.8	503	6 US-10-532-868-15	Sequence 15, Appl
16	470.5	17.5	430	7 US-11-056-355B-81092	Sequence 81092, A
17	470.5	17.5	450	7 US-11-056-355B-81091	Sequence 81091, A
18	470.5	17.5	515	7 US-11-056-355B-81090	Sequence 81090, A
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31	462	17.2	523	7 US-11-317-789A-247	Sequence 247, App
32	462	17.2	524	6 US-10-953-349-21308	Sequence 21308, A
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35	459	17.1	503	6 US-10-532-868-18	Sequence 18, Appl
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39	456.5	17.0	512	7 US-11-056-355B-83651	Sequence 83651, A
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41	451	16.8	524	6 US-10-953-349-21297	Sequence 21297, A
42	451	16.8	524	7 US-11-056-355B-60225	Sequence 60225, A
43	451	16.8	533	6 US-10-953-349-21296	Sequence 21296, A
44	451	16.8	533	7 US-11-056-355B-60224	Sequence 60224, A
45	449.5	16.7	502	6 US-10-532-868-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-10-540-310-4

; Sequence 4, Application US/10540310

; Publication No. US20060166212A1

; GENERAL INFORMATION:

; APPLICANT: Avalon Pharmaceuticals, Inc.

; TITLE OF INVENTION: Breast Specific Protein Expressed in Cancer and Methods of

; TITLE OF INVENTION: Use Thereof

; FILE REFERENCE: 689290-183

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This page gives you Search Results detail for the Application 10717296 and Search Result us-10-7:
start

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 14, 2006, 10:13:15 ; Search time 43 Seconds
 (without alignments)
 1129.988 Million cell updates/sec

Title: US-10-717-296-307

Perfect score: 2690

Sequence: 1 MEPSWLQELMAHPFLLLILL.....VRQVVLKSKNGIHVFAKKVC 505

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description
--------	-------	-----	-------	-------	--------	----	----	-------------

1	1504	55.9	507	2	JC7883			cytochrome P450 4X
2	1392	51.7	510	1	A29368			prostaglandin omega
3	1361.5	50.6	519	2	JX0331			laurate omega-hyd
4	1359.5	50.5	519	2	I53015			fatty acid omega-h
5	1357.5	50.5	509	1	O4RTLO			laurate omega-hyd
6	1351.5	50.2	511	1	A34260			laurate omega-hyd
7	1347.5	50.1	511	1	B34160			cytochrome P450 4A
8	1338	49.7	508	1	A36304			cytochrome P450 4A

9	1333.5	49.6	591	2	I65981	fatty acid omega-h
10	1333	49.6	510	1	A34160	laurate omega-hydr
11	1330.5	49.5	509	2	S47553	cytochrome P450 Cy
12	1305.5	48.5	507	1	A32966	cytochrome P450 4A
13	1301	48.4	504	1	A32965	cytochrome P450 4A
14	1236.5	46.0	511	2	S66472	cytochrome P450 4B
15	1219	45.3	506	1	A40164	cytochrome P450 4B
16	1205	44.8	511	1	B40164	cytochrome P450 4B
17	1189.5	44.2	515	1	JE0361	cytochromes P450,
18	1180.5	43.9	511	1	O4HUB1	cytochrome P450 4B
19	1016	37.8	520	2	S45702	leukotriene-B4 20-
20	1004	37.3	522	2	JC4532	cytochrome P450 4F
21	994	37.0	524	2	JC7594	cytochrome P450 en
22	994	37.0	524	2	JC7598	cytochrome P450 en
23	990	36.8	524	2	S29723	cytochrome P450 4F
24	966	35.9	520	1	A46661	leukotriene B4 ome
25	953	35.4	537	2	JC4534	cytochrome P450 4F
26	920	34.2	526	2	JC4533	cytochrome P450 4F
27	660	24.5	512	2	T13611	hypothetical prote
28	649.5	24.1	511	1	A39381	cytochrome P450 4
29	648	24.1	515	2	JC8026	cytochrome P450 en
30	628.5	23.4	511	1	S25707	cytochrome P450 4D
31	628	23.3	467	2	T21236	hypothetical prote
32	619	23.0	496	1	S41192	cytochrome P450 4D
33	600.5	22.3	513	2	JC7120	cytochrome P450 en
34	574.5	21.4	499	2	T18699	hypothetical prote
35	559	20.8	503	1	S66374	cytochrome P450 4M
36	545.5	20.3	509	2	T21512	hypothetical prote
37	543.5	20.2	503	2	T24985	hypothetical prote
38	543.5	20.2	520	2	H84663	probable cytochrom
39	535	19.9	524	2	T20471	hypothetical prote
40	526	19.6	485	1	JC5236	cytochrome P450, C
41	513.5	19.1	574	2	JC7327	cytochrome P450 en
42	505	18.8	141	2	S35610	cytochrome P450 4A
43	500	18.6	141	2	S35611	cytochrome P450 4A
44	488.5	18.2	583	2	T15644	probable cytochrom
45	487.5	18.1	503	2	JC7627	cytochrome P450 3A

ALIGNMENTS

RESULT 1
JC7883
cytochrome P450 4X1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 05-Oct-2004
C;Accession: JC7883
R;Bylund, J.; Zhang, C.; Harder, D.R.
Biochem. Biophys. Res. Commun. 296, 677-684, 2002
A;Title: Identification of a novel cytochrome P450, CYP4X1, with unique localization s
A;Reference number: JC7883; MUID:22165495; PMID:12176035
A;Accession: JC7883
A;Molecule type: mRNA
A;Residues: 1-507
A;Cross-references: UNIPROT:Q8K4D6; UNIPARC:UPI00000E837D; GB:AF439343
C;Comment: This enzyme, which is a brain specific cytochrome P450 isoform belonging to
C;Genetics:
A;Gene: cyp4x1
C;Superfamily: human cytochrome P450 CYP4B1

SCORE Search Results Details for Application 10717296 and Search Result us-10-717-296- 307.rup.

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OM protein - protein search, using sw model

Run on: October 14, 2006, 10:09:50 ; Search time 305 Seconds
(without alignments)
1531.583 Million cell updates/sec

Title: US-10-717-296-307

Perfect score: 2690

Sequence: 1 MEPSWLQELMAHPFLLLILL.....VRQVVLKSKNGIHVFAKKVC 505

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	% Match Length DB ID				Description
1	2685	99.8	505	1	CP4Z1_HUMAN	Q86w10 homo sapien
2	2685	99.8	505	2	Q5VVE4_HUMAN	Q5vve4 homo sapien
3	1727	64.2	340	2	Q8N1L4_HUMAN	Q8n1l4 homo sapien
4	1504	55.9	507	1	CP4X1_RAT	Q8k4d6 rattus norv

5	1494	55.5	507	2	Q6A152_MOUSE	Q6a152 mus musculu
6	1476	54.9	509	1	CP4X1_HUMAN	Q8n118 homo sapien
7	1476	54.9	509	2	Q5VVE5_HUMAN	Q5vve5 homo sapien
8	1468	54.6	499	2	Q8BYS0_MOUSE	Q8bys0 mus musculu
9	1459	54.2	292	2	Q66ZJ5_HUMAN	Q66zj5 homo sapien
10	1403	52.2	510	2	Q2VHZ9_CANFA	Q2vhz9 canis famil
11	1388	51.6	510	1	CP4A4_RABIT	P10611 oryctolagus
12	1383	51.4	510	2	Q2VHZ7_CANFA	Q2vhz7 canis famil
13	1382	51.4	510	2	Q2VHZ8_CANFA	Q2vhz8 canis famil
14	1361.5	50.6	509	2	Q5EBD8_RAT	Q5ebd8 rattus norv
15	1361.5	50.6	519	1	CP4AB_HUMAN	Q02928 homo sapien
16	1361.5	50.6	519	2	Q5VSP8_HUMAN	Q5vsp8 homo sapien
17	1360	50.6	508	1	CP4AC_RAT	P24464 rattus norv
18	1357.5	50.5	509	1	CP4AA_RAT	P08516 rattus norv
19	1349.5	50.2	511	1	CP4A5_RABIT	P14579 oryctolagus
20	1346	50.0	510	1	CP4A6_RABIT	P14580 oryctolagus
21	1343.5	49.9	509	1	CP4AA_MOUSE	O88833 mus musculu
22	1341.5	49.9	511	1	CP4A7_RABIT	P14581 oryctolagus
23	1339	49.8	504	2	Q9GJX5_PIG	Q9gjx5 sus scrofa
24	1338.5	49.8	516	2	Q5RFC5_PONPY	Q5rfc5 pongo pygma
25	1338.5	49.8	519	2	Q6JXK8_HUMAN	Q6jxk8 homo sapien
26	1338.5	49.8	519	2	Q5R5F7_PONPY	Q5r5f7 pongo pygma
27	1334	49.6	508	1	CP4AC_MOUSE	Q91w15 mus musculu
28	1332.5	49.5	521	2	Q16802_HUMAN	Q16802 homo sapien
29	1332	49.5	504	2	Q8SPK1_PIG	Q8spk1 sus scrofa
30	1329	49.4	504	2	Q8SPK0_PIG	Q8spk0 sus scrofa
31	1327.5	49.3	519	2	Q6JXK7_HUMAN	Q6jxk7 homo sapien
32	1327	49.3	504	2	Q95JF8_PIG	Q95jf8 sus scrofa
33	1324.5	49.2	515	2	Q4QQR3_XENTR	Q4qqr3 xenopus tro
34	1310	48.7	444	2	Q8NAZ3_HUMAN	Q8naz3 homo sapien
35	1309	48.7	508	2	Q6ZN67_HUMAN	Q6zn67 homo sapien
36	1309	48.7	510	2	Q5XG47_XENLA	Q5xg47 xenopus lae
37	1306.5	48.6	519	2	Q5TCH4_HUMAN	Q5tch4 homo sapien
38	1305.5	48.5	507	1	CP4AE_RAT	P20817 rattus norv
39	1305.5	48.5	519	2	Q9NRM4_HUMAN	Q9nrm4 homo sapien
40	1305	48.5	500	2	Q8HYL5_PHACI	Q8hy15 phascolarct
41	1301	48.4	504	1	CP4A2_RAT	P20816 rattus norv
42	1301	48.4	504	2	Q4G071_RAT	Q4g071 rattus norv
43	1287.5	47.9	507	1	CP4AE_MOUSE	O35728 mus musculu
44	1275	47.4	501	2	Q9PVV8_XENLA	Q9pvv8 xenopus lae
45	1237.5	46.0	496	2	Q6AZQ1_XENLA	Q6azq1 xenopus lae

ALIGNMENTS

RESULT 1

CP4Z1_HUMAN

ID CP4Z1_HUMAN STANDARD; PRT; 505 AA.

AC Q86W10;

DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.

DT 01-JUN-2003, sequence version 1.

DT 07-FEB-2006, entry version 25.

DE Cytochrome P450 4Z1 (EC 1.14.14.1) (CYPIVZ1).

GN Name=CYP4Z1; ORFNames=UNQ3060/PRO9882;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

(10/17/2006)

Qy	61 YPVKEFEVYHKLMEKYPACAVPLWVGPFMFFSVHDPDYAKILLKRQDPKSAVSHKILESW	120
Db	61 YPVKEFEVYHKLMEKYPACAVPLWVGPFMFFSVHDPDYAKILLKRQDPKSAVSHKILESW	120
Qy	121 VGRGLVTLDGSKWKKHRQIVKPGFNISILKIFITMMSESVRMMLNKWEERIAQNSRLELF	180
Db	121 VGRGLVTLDGSKWKKHRQIVKPGFNISILKIFITMMSESVRMMLNKWEERIAQNSRLELF	180
Qy	181 QHVSLMTLDSIMKCAFHQGSIQLDSTLDSYLKAVFNLISKISNQRMNNFLHHNDLVFKFS	240
Db	181 QHVSLMTLDSIMKCAFHQGSIQLDSTLDSYLKAVFNLISKISNQRMNNFLHHNDLVFKFS	240
Qy	241 SQGQIFSKFNQELHQFTEKVIQDRKESLKDKLKQDTTQKRRWDFLDILLSAKSENTKDFS	300
Db	241 SQGQIFSKFNQELHQFTEKVIQDRKESLKDKLKQDTTQKRRWDFLDILLSAKSENTKDFS	300
Qy	301 EADLQAEVKTFMAGHDSSAISWILYCLAKYPEHQQRCRDEIRELLGDGSSITWEHLS	360
Db	301 EADLQAEVKTFMAGHDSSAISWILYCLAKYPEHQQRCRDEIRELLGDGSSITWEHLS	360
Qy	361 QMPYTTMCIKECLRLYAPVVNISRLLDKPITFPDGRSLPAGITVFINIWALHHNPFWED	420
Db	361 QMPYTTMCIKECLRLYAPVVNISRLLDKPITFPDGRSLPAGITVFINIWALHHNPFWED	420
Qy	421 PQVFNPLRFSRENSEKIHPYAFIPFSAGLRNCIGQHFAIECKVAVALTLLRFKLAPDHS	480
Db	421 PQVFNPLRFSRENSEKIHPYAFIPFSAGLRNCIGQHFAIECKVAVALTLLRFKLAPDHS	480
Qy	481 RPPQPVRQVVLKSNGIHVFAKKVC	505
Db	481 RPPQPVRQVVLKSNGIHVFAKKVC	505

RESULT 2

AAE14447

ID AAE14447 standard; protein; 505 AA.

XX

AC AAE14447;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human drug metabolising enzyme (DME)-10.

XX

KW Human; drug metabolising enzyme; DME-10; autoimmune; inflammatory;
 KW cell proliferative; developmental; endocrine; eye; metabolic; AIDS;
 KW gastrointestinal disorder; liver disorder; cancer; arteriosclerosis;
 KW adult respiratory distress syndrome; anaemia; epilepsy; hypothyroidism;
 KW hypothalamus; pituitary; diabetes; hypogonadism; conjunctivitis;
 KW glaucoma; cystic fibrosis; hypercholesterolaemia; gastritis;
 KW peptic ulcer; hepatitis; gene therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..31

FT /label= Signal_peptide

FT Domain 14..33

FT /label= Transmembrane_domain

FT Protein 32..505

FT /label= Mature_DME-10

XX
PN WO200190334-A2.
XX
PD 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-US017150.
XX
PR 25-MAY-2000; 2000US-0207901P.
PR 01-JUN-2000; 2000US-0208983P.
PR 07-JUN-2000; 2000US-0209861P.
PR 15-JUN-2000; 2000US-0211825P.
PR 22-JUN-2000; 2000US-0213744P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Sanjanwala MS, Baughn MR, Gandhi AR, Ring HZ, Elliott V;
PI Walia NK, Yang J, Khan FA, Ramkumar J, Tang YT, Hafalia A, Lal P;
PI Nguyen DB, Yao MG, Lee EA, Tribouley CM, Patterson C, Lu Y;
PI Burford N, Ding L, Bruns CM, Kearney L, Reddy R;
XX
DR WPI; 2002-097650/13.
DR N-PSDB; AAD24015.
XX
PT New human drug metabolizing enzymes and polynucleotides encoding the
PT enzyme for diagnosing, preventing or treating cell proliferative,
PT autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal
PT disorders.
XX
PS Claim 1; Page 145-146; 158pp; English.
XX
CC The present sequence is human drug metabolising enzyme (DME)-10. DME
CC polypeptide, polynucleotide and modulators are useful for diagnosis,
CC treatment and prevention of autoimmune/inflammatory, cell proliferative,
CC developmental, endocrine, eye, metabolic, and gastrointestinal disorders,
CC including liver disorders. The autoimmune/inflammatory disorders
CC treatable include AIDS, adult respiratory distress syndrome, Addison's
CC disease, allergies, anaemia, asthma, atherosclerosis, osteoporosis,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, Crohn's disease,
CC atopic dermatitis, diabetic mellitus, Graves' disease,
CC glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, systemic sclerosis, ulcerative colitis, haemodialysis and
CC uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic
CC infections and trauma, and cell proliferative disorders such as cancer,
CC actinic keratosis, arteriosclerosis, atherosclerosis, bursitis,
CC cirrhosis, hepatitis and psoriasis. Developmental disorders include
CC anaemia, renal tubular acidosis, epilepsy, hypothyroidism and cataract,
CC and endocrine disorders include disorders of hypothalamus and pituitary,
CC disorders associated with hypopituitarism, including sarcoidosis,
CC diabetes insipidus, hypogonadism, disorders associated with
CC hypothyroidism including goitre, acute thyroiditis, Graves' disease,
CC disorders associated with hyperparathyroidism, pancreatic disorders such
CC as type I or type II diabetes mellitus, disorders associated with
CC adrenals such as hyperplasia, Cushing's disease, endometriosis,
CC infertility, hypergonadal disorders, and gynaecomastia. Eye disorders
CC include conjunctivitis, keratitis, glaucoma and macular degeneration, and
CC metabolic disorders include diabetes, cystic fibrosis, goitre,
CC hypercholesterolaemia, hypoglycaemia, hyperlipidaemia, lysosomal storage
CC diseases, obesity, phenylketonuria and hypocalcaemia. Also the molecules
CC are useful for treating gastrointestinal disorders such as dysphagia,
CC gastritis, peptic ulcer, cholelithiasis, cirrhosis, hepatitis,
CC hyperbilirubinaemia, constipation, diarrhoea, jaundice, Wilson's disease,

CC thrombosis and hepatic tumours. The DME polypeptide is also useful for
CC screening its agonist or antagonist

XX

SQ Sequence 505 AA;

Query Match 100.0%; Score 2690; DB 5; Length 505;
Best Local Similarity 100.0%; Pred. No. 1.2e-230;
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEPSWLQELMAHPFLLLILLCMSLLLQVIRLYQRRRWMIRALHLFPAPPAHWFYGHKEF 60
Db	1 MEPSWLQELMAHPFLLLILLCMSLLLQVIRLYQRRRWMIRALHLFPAPPAHWFYGHKEF 60
Qy	61 YPVKEFEVYHKLMEKYPACAVPLWVGPFITMFFSVHDPDYAKILLKRQDPKSAVSHKILESW 120
Db	61 YPVKEFEVYHKLMEKYPACAVPLWVGPFITMFFSVHDPDYAKILLKRQDPKSAVSHKILESW 120
Qy	121 VGRGLVTLDGSKKHRQIVKPGFNISILKIFITMMSEVRMMLNKWEERIAQNSRLELF 180
Db	121 VGRGLVTLDGSKKHRQIVKPGFNISILKIFITMMSEVRMMLNKWEERIAQNSRLELF 180
Qy	181 QHVSLMTLDSIMKCAFQHQGSIQLDSTLDSYLKAVFNLSKISNQRMNNFLHHNDLVFKFS 240
Db	181 QHVSLMTLDSIMKCAFQHQGSIQLDSTLDSYLKAVFNLSKISNQRMNNFLHHNDLVFKFS 240
Qy	241 SQGQIFSFKFNQELHQFTEKVIQDRKESLKDKLKQDTTQKRRWDFLDILLSAKSENTKDFS 300
Db	241 SQGQIFSFKFNQELHQFTEKVIQDRKESLKDKLKQDTTQKRRWDFLDILLSAKSENTKDFS 300
Qy	301 EADLQAEVKTFMAGHDTTSSAISWILYCLAKYPEHQQR CRDEIRELLGDGSSITWEHLS 360
Db	301 EADLQAEVKTFMAGHDTTSSAISWILYCLAKYPEHQQR CRDEIRELLGDGSSITWEHLS 360
Qy	361 QMPYTTMCIKECLRLYAPVVNISRLLDKPITFPDGRSLPAGITVFINIWAHHNPFWED 420
Db	361 QMPYTTMCIKECLRLYAPVVNISRLLDKPITFPDGRSLPAGITVFINIWAHHNPFWED 420
Qy	421 PQVFNPRLFSRENSEKIHPYAFIPFSAGLRNCIGQHFAIECKVAVALTLRFKLAPDHS 480
Db	421 PQVFNPRLFSRENSEKIHPYAFIPFSAGLRNCIGQHFAIECKVAVALTLRFKLAPDHS 480
Qy	481 RPPQPVRQVVLKSNGIHVFAKKVC 505
Db	481 RPPQPVRQVVLKSNGIHVFAKKVC 505

RESULT 3

ADU01526

ID ADU01526 standard; protein; 505 AA.

XX

AC ADU01526;

XX

DT 30-DEC-2004 (first entry)

XX

DE Breast cancer associated polypeptide seqid 307.

XX

KW cytostatic; gene therapy; vaccine; breast cancer; cancer; tumour;
KW immune response; O8E; vaccine.

XX

OS Homo sapiens.

XX